



SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: KAUFMAN, RUSSEL E.
SLENTZ-KESLER, KIMBERLY

(ii) TITLE OF INVENTION: GENE PRODUCT OVER EXPRESSED IN CANCER CELLS

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: NIXON & VANDERHYE P.C.
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(C) CITY: ARLINGTON
(D) STATE: VIRGINIA
(E) COUNTRY: U.S.A.
(F) ZIP: 22201-4714

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 10/080,522
(B) FILING DATE: 25-FEB-2002
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/539,774
(B) FILING DATE: 31-MAR-2000
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/210,474
(B) FILING DATE: 14-DEC-1998
(C) CLASSIFICATION:

(ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: WILSON, MARY J.
(B) REGISTRATION NUMBER: 32,955
(C) REFERENCE/DOCKET NUMBER: 1579-645

(x) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gln Thr Cys Pro Leu Ala Phe Pro Gly His Val Ser Gln Ala Leu
1 5 10 15

Gly Thr Leu Leu Phe Leu Ala Ala Ser Leu Ser Ala Gln Asn Glu Gly
20 25 30

Trp Asp Ser Pro Ile Cys Thr Glu Gly Val Val Ser Val Ser Trp Gly
35 40 45

Glu Asn Thr Val Met Ser Cys Asn Ile Ser Asn Ala Phe Ser His Val
50 55 60

Asn Ile Lys Leu Arg Ala His Gly Gln Glu Ser Ala Ile Phe Asn Glu
65 70 75 80

Val Ala Pro Gly Tyr Phe Ser Arg Asp Gly Trp Gln Leu Gln Val Gln
85 90 95

Gly Gly Val Ala Gln Leu Val Ile Lys Gly Ala Arg Asp Ser His Ala
100 105 110

Gly Leu Tyr Met Trp His Leu Val Gly His Gln Arg Asn Asn Arg Gln
115 120 125

Val Thr Leu Glu Val Ser Gly Ala Glu Pro Gln Ser Ala Pro Asp Thr
130 135 140

Gly Phe Trp Pro Val Pro Ala Val Val Thr Ala Val Phe Ile Leu Leu
145 150 155 160

Val Ala Leu Val Met Phe Ala Trp Tyr Arg Cys Arg Cys Ser Gln Gln
165 170 175

Arg Arg Glu Lys Lys Phe Phe Leu Leu Glu Pro Gln Met Lys Val Ala
180 185 190

Ala Leu Arg Ala Gly Ala Gln Gln Gly Leu Ser Arg Ala Ser Ala Glu
195 200 205

Leu Trp Thr Pro Asp Ser Glu Pro Thr Pro Arg Pro Leu Ala Leu Val
210 215 220

Phe Lys Pro Ser Pro Leu Gly Ala Leu Glu Leu Leu Ser Pro Gln Pro
225 230 235 240

Leu Phe Pro Tyr Ala Ala Asp Pro
245

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATTCCTGCTT CCTTTAGCGT GAACGCGGGT GCGGTGCCTC CCGTGAAATA ATAAATTACAC	60
CGTCACGCTT GTTGTGAACG CGGGTGGTTC CCGAAACTTG GAGGCTTCCC GTAAACCCAG	120
CTCCTTCCTC ATCTGGGAGG TGGGTCCCGC GCGGGTCCGC CGCCTCCTCC CTGGCCCCCTC	180
CCTCTCGTGT CTTTCATTTC CCTGGGGCTC CGGGGCGCGG AGAAGCTGCA TCCCAGAGGA	240
GCGCGTCCAG GAGCGGACCC GGGAGTGTTC CAAGAGCCAG TGACAAGGAC CAGGGGCCA	300
AGTCCCACCA GCCATGCAGA CCTGCCCCCT GGCATTCCCT GGCCACGTTT CCCAGGCCCT	360
TGGGACCCCTC CTGTTTTGG CTGCCTCCTT GAGTGCTCAG AATGAAGGCT GGGACAGCCC	420
CATCTGCACA GAGGGGGTAG TCTCTGTGTC TTGGGGCGAG AACACCGTCA TGTCTGCAA	480
CATCTCCAAC GCCTTCTCCC ATGTCAACAT CAAGCTGCGT GCCCACGGC AGGAGAGCGC	540
CATCTTCAAT GAGGTGGCTC CAGGCTACTT CTCCCCGGAC GGCTGGCAGC TCCAGGTTCA	600
GGGAGGCGTG GCACAGCTGG TGATCAAAGG CGCCCGGGAC TCCCATGCTG GGCTGTACAT	660
GTGGCACCTC GTGGGACACC AGAGAAATAA CAGACAAGTC ACGCTGGAGG TTTCAGGTGC	720
AGAACCCCCAG TCCGCCCTG ACACTGGTT CTGGCCTGTG CCAGCGGTGG TCACTGCTGT	780
CTTCATCCTC TTGGTCGCTC TGGTCATGTT CGCCTGGTAC AGGTGCCGCT GTTCCCAGCA	840
ACGCCGGGAG AAGAAGTTCT TCCTCCTAGA ACCCCAGATG AAGGTCGCAG CCCTCAGAGC	900
GGGAGCCAG CAGGGCCTGA GCAGAGCCTC CGCTGAAC TGAGACCCAG ACTCCGAGCC	960
CACCCCAAGG CCGCTGGCAC TGGTGTCAA ACCCTCACCA CTTGGAGCCC TGGAGCTGCT	1020
GTCCCCCCCAC ACCCTTGTTT CCATATGCCG CAGACCCATA GCCGCCTGCA AGGCAGAGAG	1080
GACACAGGAG AGCCAGCCCT GAGTGCCGAC CTTGGGTGGC GGGGCCTGGG TCTCTCGTCC	1140
CACCCGGAGG GCACAGACAC CGGCTTGCTT GGCAGGCTGG GCCTCTGTGT CACCCACTCC	1200
TGGGTGCGTG CAGACCCCTC CCCTCCACCC CCCAGGTCTT CCAAGCTCTG CTTCCCTCAGT	1260
TTCCAAAATG GAACCACCTC ACCTCCGCAG CACCCGACTT ACCAGGACGC ATGCCCTCC	1320
CTCTGCCCTC ATCAAACCCA CAGACCCGGA CTCCCTTCT GCCACCCAG GCTGGTCCGG	1380
CCCCAGGTGT GGGGTCCGCT CTCTCCACTC CCAGGGCTCC GCGCCCAAGT GAGGGGGCCC	1440
CTGCCGGAGC CTCAGACACA CTGGAGTTCA GGGCTGGGGG GGCCTTGGCA CATACTGTC	1500
CCTTGGCTAT GAGCAGGCTT TGGGGGCCCT TCCGCGGCAG CCCCCGGGGC CGAGGTAGGG	1560
TCTGGGGGCT TAGAGGCTGG GATGGCTCCTT GGCCCCACCG CCAGGGGCA AGCGCAGGCC	1620
GGGCTGGGAG GCGGCGGCAG CGGCTGGGC TGGGGGGTCA GGTGGACGCT GCCTCCGGG	1680
CTGGTCGCGC ATCCCTCAGT CCCTCGGCCA CCCGGGGTC GCTCCCTCGT GCCCACCGCA	1740

CCTGCCGAGC CTCTTGAC CCAGATCTGT TCATGCTTT GTCTCGTCA CTGGCGGG 1800
GCCCTTGAT GTCTCATCT GTATGGGTG GAAAAATCAC CGGAAATCCC CCTTCAGTTC 1860
TTGAAAAAG TTCCATGACT CGAATATCTG AAATGAAGAA AACAAACCGA CTCACAAACC 1920
TCCAAGTAGC TCCAAATGCA ATTTTTAAAA TGGAAAACAA AAATCTGAAA GAAACGTCTT 1980
TAGTGGCTTT AAGCCCCAAA ACGTCCCTAA GGCGTCCTCG AGATGAAGAC GGGGGGGAGC 2040
CCCAGCCAGG TGGAGACCCC GCAGGACGCG CGGGCGCCCG GTGACCGAGG CCTCGCACAG 2100
CCGGCCGCC CGGGGTCTGG GCCGAGCCAG GGTCCAAGAG GGGCGCGTTT GTGTCTCGGG 2160
TTAAAATAAG GTTCCGTCCG 2180